

Genome

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Human Chromosome 19 Closure: Status of a High-Resolution Physical Map of the q-arm

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An ordered clone map has been obtained starting from a foundation of cosmid contigs assembled by automated fingerprinting and localized to the cytogenetic map by fluorescence *in situ* hybridization (FISH). Clonal continuity of extensive regions of the map have been obtained by binning and linking the pre-mapped cosmid contigs by means of YACs. The map consists of a 184 YACs linking a framework of 113 cosmid contigs for which both order and distance are known. The number of ordered clone islands in this arm has been reduced to 22 with a coverage of approximately 28.4 Mb or 95% of the total. Thus, the average estimated gap distance among the 22 islands is 74 Kb. The largest continuous clonal coverage for this arm is a 17 Megabase region that spans the entire q12, q13.1 and q13.2 cytogenetic bands of this chromosome. It is comprised of 169 YAC members linking 165 cosmid contigs. Eighty percent, or about 13.2 Mb of the entire region spanned by this YAC-cosmid contig has been resolved to the *EcoRI* restriction map level. Twenty nine STSs associated with genetic markers or derived from FISH-mapped cosmids have been placed on the map. A total of 18 STSs derived from genetic markers have been placed on the map without a single discrepancy between the assigned genetic position of the markers and its physical localization within the YAC-cosmid contigs. This type of map provides a level of resolution two orders of magnitude higher than those obtained from YACs alone. In addition, it provides ready to use reagents for DNA sequencing.

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Oral or Poster Presentation

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